8. A method of detecting a human disease state, comprising the steps of:

a) detecting the quantity of a disease marker expressed in human peripheral blood; and

b) comparing the quantity of said marker to the quantity expressed in peripheral blood of a normal individual;

wherein a difference in quantity of expression is indicative of a disease state.

9. The method of claim 8, wherein said disease marker is an mRNA.

10. The method of claim 9, wherein said mRNA is amplified by an RNA polymerase reaction.

11. The method of claim 9, wherein said mRNA is amplified by reverse transcriptase polymerase chain reaction or the ligase chain reaction.

12. The method of claim 8, wherein said detecting is by RNA fingerprinting, branched DNA or a nuclease protection assay.

13. The method of claim 8, wherein the disease state is metastatic cancer, asthma, lupus erythromatosis, rheumatoid arthritis, multiple sclerosis, myasthenia gravis, autoimmune thyroiditis, ALS (Lou Gehrig's disease), interstitial cystitis or prostatitis.

14. The method of claim 8 wherein the disease state is metastatic cancer.

15. The method of claim 14 wherein the metastatic cancer is metastatic prostate cancer.

16. The method of claim 14 wherein the metastatic cancer is metastatic breast cancer.

17. The method of claim 9 in which said mRNA comprises one or more of the sequences or the complements of the sequences disclosed herein as SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:29, SEQ ID NO:34, SEQ ID NO:48 or SEQ ID NO:49.

18. The method of claim 8 in which said marker is a product of an interleukin 8 (IL-8) or interleukin 10 (IL-10) gene.

19. The method of claim 9, further comprising the steps of

a) providing primers that selectively amplify said disease state marker;

b) amplifying said nucleic acid with said primers to form nucleic acid amplification products;

c) detecting said nucleic acid amplification products; and

d) measuring the amount of said nucleic acid amplification products formed.

20. The method of claim 19 in which said primers are selected to specifically amplify a nucleic acid having a sequence comprising SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:29, SEQ ID NO:34, SEQ ID NO:48 or SEQ ID NO:49.

21. The method of claim 8, wherein said marker is a polypeptide.

22. The method of claim 21, wherein said polypeptide is encoded by a nucleic acid sequence comprising the sequence disclosed herein SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:29, SEQ ID NO:34, SEQ ID NO:48 or SEQ ID NO:49.

23. The method of claim 21, wherein said detection is by an antibody immunoreactive with said marker.

24. The method of claim 21, wherein said polypeptide is encoded by an IL-8 or IL-10 gene.

25. The method of claim 8, wherein said marker is a product of the IL-8 gene and wherein said comparison is between two alternatively spliced forms of an IL-8 gene product.

26. The method of claim 24, wherein the quantity of IL-8 polypeptide in peripheral blood is measured using an *in vitro* bioassay that detects an IL-8 mediated biological process.

64. The method of claim 19, in which said primers are selected to specifically amplify a nucleic acid product of the IL-10 gene.

65. The method of claim 24, wherein the quantity of IL-10 polypeptide in peripheral blood is measured using an *in vitro* bioassay that detects at least one IL-10 mediated biological process.